

P4/10

# CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/510,408

CRF Edit Date: 10/19/04  
Edited by: AZ

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted: / invalid beginning/end-of-file text ; / page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

\_\_\_ Other:

\_\_\_\_\_  
\_\_\_\_\_  
\_\_\_\_\_



PCT

## RAW SEQUENCE LISTING

DATE: 10/19/2004

PATENT APPLICATION: US/10/510,408

TIME: 14:41:00

Input Set : N:\AMC\PTO.AMC.txt

Output Set: N:\CRF4\10192004\J510408.raw

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3 <110> APPLICANT: Jorgensen, Steen Troels
4      Olsen, Peter Bjarke
5      Andersen, Jens Tonne
6      Rasmussen, Michael Dolberg
8 <120> TITLE OF INVENTION: Improved Bacillus Host Cell
10 <130> FILE REFERENCE: 10295.204-US
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/510,408
C--> 12 <141> CURRENT FILING DATE: 2004-10-05
12 <160> NUMBER OF SEQ ID NOS: 191
14 <170> SOFTWARE: PatentIn version 3.3
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1055
18 <212> TYPE: DNA
19 <213> ORGANISM: Bacillus licheniformis
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (34)..(552)
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28                               Met Tyr Ser Arg Ser Lys Phe
29                               1           5
31 aaa atc ggt tta ttg ctt att gga agt ctg ctg gcc gcg ctc agc ttt      102
32 Lys Ile Gly Leu Leu Leu Ile Gly Ser Leu Leu Ala Ala Leu Ser Phe
33      10           15           20
35 cac ctg gag gcc ttg gcc gaa aag ccg gct aaa gtt caa atc cag ctt      150
36 His Leu Glu Ala Leu Ala Glu Lys Pro Ala Lys Val Gln Ile Gln Leu
37      25           30           35
39 gaa aag gtt tat ctg gac gga gac gtt gga att gag aat aaa gta gag      198
40 Glu Lys Val Tyr Leu Asp Gly Asp Val Gly Ile Glu Asn Lys Val Glu
41 40           45           50           55
43 gcc gct cgc aca ctg gaa gac ttt aaa gct gct tat aaa ggg tgg cag      246
44 Ala Ala Arg Thr Leu Glu Asp Phe Lys Ala Ala Tyr Lys Gly Trp Gln
45      60           65           70
47 ctc atc gat cag aaa aag ggg ttt att ctg ttt cgc aaa cag gtg gac      294
48 Leu Ile Asp Gln Lys Lys Gly Phe Ile Leu Phe Arg Lys Gln Val Asp
49      75           80           85
51 gac att tct ccc ctc agc aaa aca aac ggt tat atc gga gtg act gaa      342
52 Asp Ile Ser Pro Leu Ser Lys Thr Asn Gly Tyr Ile Gly Val Thr Glu
53      90           95           100
55 gat ggc gtg att tcg act ttt cac ggt cgc ccg ggc atc tta tca gaa      390
56 Asp Gly Val Ile Ser Thr Phe His Gly Arg Pro Gly Ile Leu Ser Glu
57      105           110           115
59 ccc att caa tcg ttt ttt cag att gat ata aag cgg ctg gaa agc cgg      438

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61 120 125 130 135
63 atg gcg gat gat ctg cgc aaa ggg ata cca tac cgc acg aaa aag gaa 486
64 Met Ala Asp Asp Leu Arg Lys Gly Ile Pro Tyr Arg Thr Lys Lys Glu
65 140 145 150
67 ttt gaa cat gtc att gaa gcc gta aaa tca tcc gga agc caa cat cat 534
68 Phe Glu His Val Ile Glu Ala Val Lys Ser Ser Gly Ser Gln His His
69 155 160 165
71 gta gaa gat atg aag aca tgacgctggt atgtcttttt tcagctgcag 582
72 Val Glu Asp Met Lys Thr
73 170
75 acagaagctt ttttagcgaa catatgttaa ctttttcatt ctagctttgc ctgttttgtg 642
77 ttacaatgaa gagcagtcaa agaggtgaat gaacgttgat cgaattcgta aaagggacga 702
79 ttgattatgt atcgcccaa tatattgtca ttgaaaacgg cgggatcggc tatcagatct 762
81 tcacgcaaaa tccgtttatt tataagaaaa acagcaaaga aacaatctat acataccatt 822
83 atgtaagaga agacacgaat gcgctgtacg gcttttcgac aaggaagaa aaaatgctgt 882
85 ttacgaaaat gctgaatgtt acggggatcg gcccaaaagg agcgcttgcg atcctcgctt 942
87 ccggcgatcc gggagcgggtg attgaagcga tcgagaatga ggacgaagca tttctcgctca 1002
89 aatttcccg cgtaggcaaa aaaacggcaa ggcagatcat cttgacctg aaa 1055
92 <210> SEQ ID NO: 2
93 <211> LENGTH: 173
94 <212> TYPE: PRT
95 <213> ORGANISM: Bacillus licheniformis
97 <400> SEQUENCE: 2
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100 1 5 10 15
103 Leu Leu Ala Ala Leu Ser Phe His Leu Glu Ala Leu Ala Glu Lys Pro
104 20 25 30
107 Ala Lys Val Gln Ile Gln Leu Glu Lys Val Tyr Leu Asp Gly Asp Val
108 35 40 45
111 Gly Ile Glu Asn Lys Val Glu Ala Ala Arg Thr Leu Glu Asp Phe Lys
112 50 55 60
115 Ala Ala Tyr Lys Gly Trp Gln Leu Ile Asp Gln Lys Lys Gly Phe Ile
116 65 70 75 80
119 Leu Phe Arg Lys Gln Val Asp Asp Ile Ser Pro Leu Ser Lys Thr Asn
120 85 90 95
123 Gly Tyr Ile Gly Val Thr Glu Asp Gly Val Ile Ser Thr Phe His Gly
124 100 105 110
127 Arg Pro Gly Ile Leu Ser Glu Pro Ile Gln Ser Phe Phe Gln Ile Asp
128 115 120 125
131 Ile Lys Arg Leu Glu Ser Arg Met Ala Asp Asp Leu Arg Lys Gly Ile
132 130 135 140
135 Pro Tyr Arg Thr Lys Lys Glu Phe Glu His Val Ile Glu Ala Val Lys
136 145 150 155 160
139 Ser Ser Gly Ser Gln His His Val Glu Asp Met Lys Thr
140 165 170
143 <210> SEQ ID NO: 3
144 <211> LENGTH: 2130
145 <212> TYPE: DNA

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Input Set : N:\AMC\PTO.AMC.txt

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146 <213> ORGANISM: Bacillus licheniformis
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (501)..(2039)
153 <400> SEQUENCE: 3
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156 tcatattccc atcatggtaa acgaggccgg acagaaagaa aaacagcggc atatgaaatg      120
158 cgaaaatgaa cgttttcagc caatccggcg tcggtgtatg gcccaatacg accaatataa      180
160 ttcccacgcc tttcgaaaca tcaatccact ctattctttt ctgcaacacg ggtatctcct      240
162 ttcagaccgc ttgcgcccat aagaaagggt ttacacataa tgtaccatca tccccgcctt      300
164 tcttctctcg cgaatcacgc ctcaaggcga tttttaatcg tcaggaaata tttgttcat      360
166 cttcttgtaa tgategatgc tattttttta catactcagc acatactgcg tttcttattc      420
168 tcatcatgag gaaccagacc atgcaaccgc tcttataatg taatgatctt ttcatcagaa      480
170 caaaagagga caggtgaaac atg aaa ctt gaa aaa ttc gtt gac cgg ctc ccc      533
171 Met Lys Leu Glu Lys Phe Val Asp Arg Leu Pro
172          1          5          10
174 att ccg caa gtg ctt caa ccc caa agc aaa agc aag gaa atg acc tat      581
175 Ile Pro Gln Val Leu Gln Pro Gln Ser Lys Ser Lys Glu Met Thr Tyr
176          15          20          25
178 tat gaa gtc acc atg aaa gaa ttt cag cag cag ctt cac cgc gat ctg      629
179 Tyr Glu Val Thr Met Lys Glu Phe Gln Gln Gln Leu His Arg Asp Leu
180          30          35          40
182 ccg ccg act cgg ctg ttt gga tat aac gga gtt tat ccc ggc cct acc      677
183 Pro Pro Thr Arg Leu Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr
184          45          50          55
186 ttc gaa gtg cag aaa cac gaa aaa gtc gca gtc aag tgg tta aat aag      725
187 Phe Glu Val Gln Lys His Glu Lys Val Ala Val Lys Trp Leu Asn Lys
188 60          65          70          75
190 ctt ccg gat cgc cat ttt ctc ccc gtc gac cat acg ctt cac gat gac      773
191 Leu Pro Asp Arg His Phe Leu Pro Val Asp His Thr Leu His Asp Asp
192          80          85          90
194 ggc cat cac gaa cat gaa gtg aag acg gtc gtt cat ttg cac gga ggc      821
195 Gly His His Glu His Glu Val Lys Thr Val Val His Leu His Gly Gly
196          95          100          105
198 tgt acg cct gct gac agc gac gga tat cct gag gct tgg tac aca aaa      869
199 Cys Thr Pro Ala Asp Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys
200          110          115          120
202 gac ttc cat gca aaa ggc cct ttc ttt gaa agg gag gtg tat gaa tat      917
203 Asp Phe His Ala Lys Gly Pro Phe Phe Glu Arg Glu Val Tyr Glu Tyr
204          125          130          135
206 ccg aat gag cag gat gct aca gct ctt tgg tat cat gac cat gca atg      965
207 Pro Asn Glu Gln Asp Ala Thr Ala Leu Trp Tyr His Asp His Ala Met
208 140          145          150          155
210 gcc atc aca agg ctg aat gta tat gcg ggg ctt gtc ggt tta tat ttt      1013
211 Ala Ile Thr Arg Leu Asn Val Tyr Ala Gly Leu Val Gly Leu Tyr Phe
212          160          165          170
214 att cgc gac agg gaa gag cgt tca ttg aac ttg ccg aag gga gaa tat      1061
215 Ile Arg Asp Arg Glu Glu Arg Ser Leu Asn Leu Pro Lys Gly Glu Tyr
216          175          180          185

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218	gaa	atc	ccg	ctt	ttg	att	cag	gat	aaa	tca	ttt	cat	gaa	gat	ggt	tca	1109
219	Glu	Ile	Pro	Leu	Leu	Ile	Gln	Asp	Lys	Ser	Phe	His	Glu	Asp	Gly	Ser	
220			190					195					200				
222	ttg	ttt	tat	ccg	cgg	cag	cct	gac	aac	cct	tcg	ccg	gat	ctt	ccg	gac	1157
223	Leu	Phe	Tyr	Pro	Arg	Gln	Pro	Asp	Asn	Pro	Ser	Pro	Asp	Leu	Pro	Asp	
224		205					210						215				
226	ccg	tcg	att	gtt	ccg	gct	ttt	tgc	ggt	gat	acc	att	tta	gtc	aac	ggc	1205
227	Pro	Ser	Ile	Val	Pro	Ala	Phe	Cys	Gly	Asp	Thr	Ile	Leu	Val	Asn	Gly	
228	220					225					230					235	
230	aag	gta	tgg	cct	ttc	gct	gaa	ctg	gaa	ccc	cga	aaa	tac	cgt	ttt	cgg	1253
231	Lys	Val	Trp	Pro	Phe	Ala	Glu	Leu	Glu	Pro	Arg	Lys	Tyr	Arg	Phe	Arg	
232				240						245					250		
234	ata	ctg	aac	gcc	tcc	aat	acg	aga	atc	ttt	gag	ctg	tat	ttc	gat	cat	1301
235	Ile	Leu	Asn	Ala	Ser	Asn	Thr	Arg	Ile	Phe	Glu	Leu	Tyr	Phe	Asp	His	
236			255						260					265			
238	gac	atc	aca	tgt	cat	caa	atc	ggc	acg	gac	ggc	ggt	ctt	ctg	cag	cat	1349
239	Asp	Ile	Thr	Cys	His	Gln	Ile	Gly	Thr	Asp	Gly	Gly	Leu	Leu	Gln	His	
240			270					275					280				
242	ccg	gtc	aaa	gtc	aat	gaa	ctg	gtg	atc	gcg	ccg	gct	gaa	agg	tgc	gat	1397
243	Pro	Val	Lys	Val	Asn	Glu	Leu	Val	Ile	Ala	Pro	Ala	Glu	Arg	Cys	Asp	
244		285					290					295					
246	atc	atc	gtt	gat	ttt	tca	cga	gca	gaa	gga	aaa	acc	gtg	aca	ctg	aaa	1445
247	Ile	Ile	Val	Asp	Phe	Ser	Arg	Ala	Glu	Gly	Lys	Thr	Val	Thr	Leu	Lys	
248	300					305					310					315	
250	aaa	cgg	atc	ggc	tgc	ggc	gga	caa	gac	gca	gat	ccc	gat	act	gat	gcc	1493
251	Lys	Arg	Ile	Gly	Cys	Gly	Gly	Gln	Asp	Ala	Asp	Pro	Asp	Thr	Asp	Ala	
252				320						325					330		
254	gac	atc	atg	caa	ttc	cgc	atc	tca	aaa	cct	ttg	aag	caa	aaa	gat	aca	1541
255	Asp	Ile	Met	Gln	Phe	Arg	Ile	Ser	Lys	Pro	Leu	Lys	Gln	Lys	Asp	Thr	
256			335						340					345			
258	agt	tca	ttg	ccg	aga	ata	ttg	aga	aag	cgc	cca	ttt	tac	cgg	aga	cac	1589
259	Ser	Ser	Leu	Pro	Arg	Ile	Leu	Arg	Lys	Arg	Pro	Phe	Tyr	Arg	Arg	His	
260			350					355					360				
262	aag	atc	aat	gcc	ctc	aga	aat	ctg	tca	ttg	ggc	gcg	gcc	gtt	gac	caa	1637
263	Lys	Ile	Asn	Ala	Leu	Arg	Asn	Leu	Ser	Leu	Gly	Ala	Ala	Val	Asp	Gln	
264		365					370					375					
266	tat	gga	aga	cct	gtt	ctg	ctt	tta	aac	aac	aca	aag	tgg	cat	gaa	ccg	1685
267	Tyr	Gly	Arg	Pro	Val	Leu	Leu	Leu	Asn	Asn	Thr	Lys	Trp	His	Glu	Pro	
268	380					385					390				395		
270	gta	acc	gaa	aca	ccc	gca	ctc	ggc	agc	act	gag	atc	tgg	tcg	atc	atc	1733
271	Val	Thr	Glu	Thr	Pro	Ala	Leu	Gly	Ser	Thr	Glu	Ile	Trp	Ser	Ile	Ile	
272				400						405					410		
274	aat	gcc	gga	agg	gcg	atc	cat	ccg	atc	cat	tta	cat	ctt	gtt	caa	ttt	1781
275	Asn	Ala	Gly	Arg	Ala	Ile	His	Pro	Ile	His	Leu	His	Leu	Val	Gln	Phe	
276			415						420					425			
278	atg	att	ctc	gac	cac	cgg	ccg	ttt	gat	atc	gag	cgg	tat	cag	gaa	aac	1829
279	Met	Ile	Leu	Asp	His	Arg	Pro	Phe	Asp	Ile	Glu	Arg	Tyr	Gln	Glu	Asn	
280			430					435					440				
282	gga	gaa	ctt	gtt	ttt	acc	ggt	ccg	gca	gtt	cct	ccg	gca	ccg	aat	gaa	1877

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Input Set : N:\AMC\PTO.AMC.txt

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283 Gly Glu Leu Val Phe Thr Gly Pro Ala Val Pro Pro Ala Pro Asn Glu
284      445      450      455
286 aag ggg ctg aaa gac acc gtc aaa gta ccc ccg ggt tca gtg acg cgc      1925
287 Lys Gly Leu Lys Asp Thr Val Lys Val Pro Pro Gly Ser Val Thr Arg
288 460      465      470      475
290 att atc gcc acc ttt gcg ccg tac agc ggc aga tat gtt tgg cac tgc      1973
291 Ile Ile Ala Thr Phe Ala Pro Tyr Ser Gly Arg Tyr Val Trp His Cys
292      480      485      490
294 cac atc ctt gag cac gaa gat tac gat atg atg cgc cct ctt gaa gtg      2021
295 His Ile Leu Glu His Glu Asp Tyr Asp Met Met Arg Pro Leu Glu Val
296      495      500      505
298 aca gat gtt cgt cat caa taagaaaaag cctccgcatt tggaggcttt      2069
299 Thr Asp Val Arg His Gln
300      510
302 taaaaaagca caaatcatca aaaaaacccat cgctgaatcc tgtacaatat tgcacccagg      2129
304 c      2130
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 513
309 <212> TYPE: PRT
310 <213> ORGANISM: Bacillus licheniformis
312 <400> SEQUENCE: 4
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315 1      5      10      15
318 Gln Pro Gln Ser Lys Ser Lys Glu Met Thr Tyr Tyr Glu Val Thr Met
319      20      25      30
322 Lys Glu Phe Gln Gln Gln Leu His Arg Asp Leu Pro Pro Thr Arg Leu
323      35      40      45
326 Phe Gly Tyr Asn Gly Val Tyr Pro Gly Pro Thr Phe Glu Val Gln Lys
327 50      55      60
330 His Glu Lys Val Ala Val Lys Trp Leu Asn Lys Leu Pro Asp Arg His
331 65      70      75      80
334 Phe Leu Pro Val Asp His Thr Leu His Asp Asp Gly His His Glu His
335      85      90      95
338 Glu Val Lys Thr Val Val His Leu His Gly Gly Cys Thr Pro Ala Asp
339      100      105      110
342 Ser Asp Gly Tyr Pro Glu Ala Trp Tyr Thr Lys Asp Phe His Ala Lys
343      115      120      125
346 Gly Pro Phe Phe Glu Arg Glu Val Tyr Glu Tyr Pro Asn Glu Gln Asp
347      130      135      140
350 Ala Thr Ala Leu Trp Tyr His Asp His Ala Met Ala Ile Thr Arg Leu
351 145      150      155      160
354 Asn Val Tyr Ala Gly Leu Val Gly Leu Tyr Phe Ile Arg Asp Arg Glu
355      165      170      175
358 Glu Arg Ser Leu Asn Leu Pro Lys Gly Glu Tyr Glu Ile Pro Leu Leu
359      180      185      190
362 Ile Gln Asp Lys Ser Phe His Glu Asp Gly Ser Leu Phe Tyr Pro Arg
363      195      200      205
366 Gln Pro Asp Asn Pro Ser Pro Asp Leu Pro Asp Pro Ser Ile Val Pro
367      210      215      220

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/510,408

DATE: 10/19/2004

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date